

SEQUENCE LISTING

<110> Fox, Brian A.
 Gao, Zeren
 Shoemaker, Kimberly E.

<120> NEUROPILIN HOMOLOG ZCUB5

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<151> 2000-11-15

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Thr Tyr Pro Asn His Thr Val Cys Glu Lys Thr Ile Thr Val Pro Lys	
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Gly Lys Arg Leu Ile Leu Arg Leu Gly Asp Leu Asp Ile Glu Ser Gln	
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Gly Pro Tyr Cys Gly Ser Met Thr Val Pro Lys Glu Leu Leu Leu Asn	
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Ala Arg His Gln Ser Ala Glu Phe Thr Ile Ser Tyr Asp Asn Glu Lys	
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 225 230 235 240
 Gly Ser Leu Ser Asp Lys Arg Phe Leu Phe Thr Ser Asn Gly Cys Ser
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 Arg Ser Leu Ser Phe Glu Pro Asp Gly Gln Ile Arg Ala Ser Ser Ser
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 Trp Gln Ser Val Asn Glu Ser Gly Asp Gln Val His Trp Ser Pro Gly
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 Lys Lys Lys Ile Thr Gly Ile Arg Thr Thr Gly Ser Thr Gln Ser Asn
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 Glu Thr Ser Thr Gly Ile Asn Ile Thr Thr Val Ala Ile Pro Leu Val
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 Pro Val Ala Gly Val Gly Ala Gln Asp Gly Asp Tyr Gln Arg Pro His
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 Ser Ala Gln Pro Ala Asp Arg Gly Tyr Asp Arg Pro Lys Ala Val Ser
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 Ala Leu Ala Thr Glu Ser Gly His Pro Asp Ser Gln Lys Pro Pro Thr
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Gly Cys Gly His Ile Val Thr Ser Gln Asp Ser Gly Thr Met Thr Ser	
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aag aat tat cca ggg act tac ccc aat tac act gtg tgt gaa aag atc	314
Lys Asn Tyr Pro Gly Thr Tyr Pro Asn Tyr Thr Val Cys Glu Lys Ile	
50 55 60	
atc aca gtc cca aag ggg aag aga ctt att ctg agg ttg gga gat ttg	362
Ile Thr Val Pro Lys Gly Lys Arg Leu Ile Leu Arg Leu Gly Asp Leu	
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Ala Thr Asp Gln Tyr Gly Pro Tyr Cys Gly Ser Trp Ala Val Pro Lys	
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Asp Ile Ser Gly Asn Thr Lys Asp Gly Tyr Arg Asp Thr Ser Leu Leu	
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Tyr Pro Gly Thr Tyr Pro Asn Tyr Thr Val Cys Glu Lys Ile Ile Thr
      50             55             60
Val Pro Lys Gly Lys Arg Leu Ile Leu Arg Leu Gly Asp Leu Asn Ile
      65             70             75             80
Glu Ser Lys Thr Cys Ala Ser Asp Tyr Leu Leu Phe Ser Ser Ala Thr
      85             90             95
Asp Gln Tyr Gly Pro Tyr Cys Gly Ser Trp Ala Val Pro Lys Glu Leu
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			180					185					190		
Ala	Ala	Ile	His	Ala	Gly	Ile	Ile	Thr	Asp	Glu	Leu	Gly	Gly	His	Ile
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Phe	Thr	Thr	Pro	Gly	Met	Asn	Ile	Thr	Thr	Val	Ala	Ile	Pro	Ser	Val
				245					250					255	
Ile	Phe	Ile	Ala	Leu	Leu	Leu	Thr	Gly	Met	Gly	Ile	Phe	Ala	Ile	Cys
			260					265					270		
Arg	Lys	Arg	Lys	Lys	Lys	Gly	Asn	Pro	Tyr	Val	Ser	Ala	Asp	Ala	Gln
		275					280					285			
Lys	Thr	Gly	Cys	Trp	Lys	Gln	Ile	Lys	Tyr	Pro	Phe	Ala	Arg	His	Gln
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Lys	Leu	Asp	Leu	Ile	Thr	Ser	Asp	Met	Ala	Asp	Tyr	Gln	Gln	Pro	Leu
				325					330					335	
Met	Ile	Gly	Thr	Gly	Thr	Val	Ala	Arg	Lys	Gly	Ser	Thr	Phe	Arg	Pro
			340					345					350		
Met	Asp	Thr	Asp	Thr	Glu	Glu	Val	Arg	Val	Asn	Thr	Glu	Ala	Ser	Gly
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His	Tyr	Asp	Cys	Pro	His	Arg	Pro	Gly	Arg	His	Glu	Tyr	Ala	Leu	Pro
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Leu	Leu	Arg	Ala	His	Thr	Phe	Ser	Thr	Gln	Ser	Gly	Tyr	Arg	Val	Pro
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 Met Gly Thr
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ggg gct ggt ggg ccg agt gtc ctg gcg ctg ctg ttc gcc gtg tgt gct 166
 Gly Ala Gly Gly Pro Ser Val Leu Ala Leu Leu Phe Ala Val Cys Ala
 5 10 15

ccg ctc cgg ttg cag gcg gag gag ctg ggt gat ggc tgt ggg cac ata 214
 Pro Leu Arg Leu Gln Ala Glu Glu Leu Gly Asp Gly Cys Gly His Ile
 20 25 30 35

gtg acc tct cag gac agt ggc aca atg aca tct aag aat tat cca ggg 262
 Val Thr Ser Gln Asp Ser Gly Thr Met Thr Ser Lys Asn Tyr Pro Gly
 40 45 50

act tac ccc aat tac act gtg tgt gaa aag atc atc aca gtc cca aag 310
 Thr Tyr Pro Asn Tyr Thr Val Cys Glu Lys Ile Ile Thr Val Pro Lys
 55 60 65

ggg aag aga ctt att ctg agg ttg gga gat ttg aac att gag tcc aag 358
 Gly Lys Arg Leu Ile Leu Arg Leu Gly Asp Leu Asn Ile Glu Ser Lys
 70 75 80

acc tgc gct tct gac tat ctc ctc ttc agc agt gca aca gat cag tat 406
 Thr Cys Ala Ser Asp Tyr Leu Leu Phe Ser Ser Ala Thr Asp Gln Tyr
 85 90 95

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gat tta ata acc tgt ttg gaa cga ggc agc cat tat ttc gag gaa aaa	454
Asp Leu Ile Thr Cys Leu Glu Arg Gly Ser His Tyr Phe Glu Glu Lys	
100 105 110 115	
tac agc aaa ttc tgc cca gct ggc tgt aga gac ata gca gga gat att	502
Tyr Ser Lys Phe Cys Pro Ala Gly Cys Arg Asp Ile Ala Gly Asp Ile	
120 125 130	
tct ggg aat aca aaa gat ggt tac aga gat acc tct tta ttg tgc aaa	550
Ser Gly Asn Thr Lys Asp Gly Tyr Arg Asp Thr Ser Leu Leu Cys Lys	
135 140 145	
gct gcc atc cac gca ggg atc atc aca gat gaa cta ggt ggc cac atc	598
Ala Ala Ile His Ala Gly Ile Ile Thr Asp Glu Leu Gly Gly His Ile	
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aac ttg ctt cag agc aaa ggg ata agt cac tat gaa gga ctc ctg gcc	646
Asn Leu Leu Gln Ser Lys Gly Ile Ser His Tyr Glu Gly Leu Leu Ala	
165 170 175	
aat ggc gtg ctc tcc cgg cat ggt tct ttg tcg gaa aag cga ttt ctt	694
Asn Gly Val Leu Ser Arg His Gly Ser Leu Ser Glu Lys Arg Phe Leu	
180 185 190 195	
ttt aca acc cca gga atg aat att aca act gtg gcg att cca tca gtg	742
Phe Thr Thr Pro Gly Met Asn Ile Thr Thr Val Ala Ile Pro Ser Val	
200 205 210	
atc ttc atc gcc ctc ctt ctg act gga atg ggg atc ttt gca atc tgt	790
Ile Phe Ile Ala Leu Leu Leu Thr Gly Met Gly Ile Phe Ala Ile Cys	
215 220 225	
aga aag agg aaa aag aaa gga aat cca tat gtg tca gct gac gct cag	838
Arg Lys Arg Lys Lys Lys Gly Asn Pro Tyr Val Ser Ala Asp Ala Gln	
230 235 240	
aaa aca ggc tgt tgg aag cag att aaa tat ccc ttt gcc agg cat cag	886
Lys Thr Gly Cys Trp Lys Gln Ile Lys Tyr Pro Phe Ala Arg His Gln	
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tcg acg gaa ttt acc atc agc tat gac aat gaa aaa gag atg aca caa	934
Ser Thr Glu Phe Thr Ile Ser Tyr Asp Asn Glu Lys Glu Met Thr Gln	
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aag ttg gat ctc atc act agt gat atg gca gat tat cag cag cct ctc	982
Lys Leu Asp Leu Ile Thr Ser Asp Met Ala Asp Tyr Gln Gln Pro Leu	
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Met Ile Gly Thr Gly Thr Val Ala Arg Lys Gly Ser Thr Phe Arg Pro	
295 300 305	
atg gac aca gac act gag gag gtc aga gtg aac act gag gcc agc ggc	1078
Met Asp Thr Asp Thr Glu Glu Val Arg Val Asn Thr Glu Ala Ser Gly	
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cac tat gac tgt cct cac cgc ccg ggc cgc cat gag tac gca ctg cct	1126
His Tyr Asp Cys Pro His Arg Pro Gly Arg His Glu Tyr Ala Leu Pro	
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Leu Leu Arg Ala His Thr Phe Ser Thr Gln Ser Gly Tyr Arg Val Pro	
360 365 370	
ggg ccc agg ccc act cac aaa cac tcc cat tcc tct gga ggc ttt cct	1270
Gly Pro Arg Pro Thr His Lys His Ser His Ser Ser Gly Gly Phe Pro	
375 380 385	
cct gct aca gga gcc acc cag gtt gaa agc tat cag agg cca gca agc	1318
Pro Ala Thr Gly Ala Thr Gln Val Glu Ser Tyr Gln Arg Pro Ala Ser	
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ccc aag cct gtg ggt ggt ggc tat gac aag cct gct gct agc agc ttc	1366
Pro Lys Pro Val Gly Gly Gly Tyr Asp Lys Pro Ala Ala Ser Ser Phe	
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ttg gac agc aga gac cca gcc tct cag tca cag atg act tcc ggg gga	1414
Leu Asp Ser Arg Asp Pro Ala Ser Gln Ser Gln Met Thr Ser Gly Gly	
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 Thr Ala Met Thr Ala Leu Leu *
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Gly His Ile Val Thr Ser Gln Asp Ser Gly Thr Met Thr Ser Lys Asn
 35 40 45
 Tyr Pro Gly Thr Tyr Pro Asn Tyr Thr Val Cys Glu Lys Ile Ile Thr
 50 55 60
 Val Pro Lys Gly Lys Arg Leu Ile Leu Arg Leu Gly Asp Leu Asn Ile
 65 70 75 80
 Glu Ser Lys Thr Cys Ala Ser Asp Tyr Leu Leu Phe Ser Ser Ala Thr
 85 90 95
 Asp Gln Tyr Asp Leu Ile Thr Cys Leu Glu Arg Gly Ser His Tyr Phe
 100 105 110
 Glu Glu Lys Tyr Ser Lys Phe Cys Pro Ala Gly Cys Arg Asp Ile Ala
 115 120 125
 Gly Asp Ile Ser Gly Asn Thr Lys Asp Gly Tyr Arg Asp Thr Ser Leu
 130 135 140
 Leu Cys Lys Ala Ala Ile His Ala Gly Ile Ile Thr Asp Glu Leu Gly
 145 150 155 160
 Gly His Ile Asn Leu Leu Gln Ser Lys Gly Ile Ser His Tyr Glu Gly
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 Leu Leu Ala Asn Gly Val Leu Ser Arg His Gly Ser Leu Ser Glu Lys
 180 185 190
 Arg Phe Leu Phe Thr Thr Pro Gly Met Asn Ile Thr Thr Val Ala Ile
 195 200 205
 Pro Ser Val Ile Phe Ile Ala Leu Leu Leu Thr Gly Met Gly Ile Phe
 210 215 220
 Ala Ile Cys Arg Lys Arg Lys Lys Lys Gly Asn Pro Tyr Val Ser Ala
 225 230 235 240
 Asp Ala Gln Lys Thr Gly Cys Trp Lys Gln Ile Lys Tyr Pro Phe Ala
 245 250 255
 Arg His Gln Ser Thr Glu Phe Thr Ile Ser Tyr Asp Asn Glu Lys Glu
 260 265 270
 Met Thr Gln Lys Leu Asp Leu Ile Thr Ser Asp Met Ala Asp Tyr Gln
 275 280 285
 Gln Pro Leu Met Ile Gly Thr Gly Thr Val Ala Arg Lys Gly Ser Thr
 290 295 300
 Phe Arg Pro Met Asp Thr Asp Thr Glu Glu Val Arg Val Asn Thr Glu
 305 310 315 320
 Ala Ser Gly His Tyr Asp Cys Pro His Arg Pro Gly Arg His Glu Tyr
 325 330 335
 Ala Leu Pro Leu Thr His Ser Glu Pro Glu Tyr Ala Thr Pro Ile Val
 340 345 350
 Glu Arg His Leu Leu Arg Ala His Thr Phe Ser Thr Gln Ser Gly Tyr
 355 360 365

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Arg Val Pro Gly Pro Arg Pro Thr His Lys His Ser His Ser Ser Gly
 370 375 380
 Gly Phe Pro Pro Ala Thr Gly Ala Thr Gln Val Glu Ser Tyr Gln Arg
 385 390 395 400
 Pro Ala Ser Pro Lys Pro Val Gly Gly Gly Tyr Asp Lys Pro Ala Ala
 405 410 415
 Ser Ser Phe Leu Asp Ser Arg Asp Pro Ala Ser Gln Ser Gln Met Thr
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<223> Xaa is any amino acid

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<222> (10)...(13)

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<222> (14)...(14)

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<222> (15)...(15)

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<223> Xaa is Ile, Leu, Phe, Val, Ser or Tyr

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<222> (17)...(17)

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<223> Xaa is Ser, Thr, Ala, His or Asn

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<222> (19)...(19)

<223> Xaa is Pro, Leu, Ala or Ile

<221> VARIANT

<222> (20)...(20)

<223> Xaa is Asn, Ser, Glu, Asp or His

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<222> (21)...(21)

<223> Xaa is Tyr, Phe, Trp and Gly

<221> VARIANT

<222> (22)...(22)

<223> Xaa is Pro, Ile or Gly

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FOSTT-2ET200T

<222> (23)...(23)

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FOSTT#2ETEDDT

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Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa
			20					25							30		
Xaa	Xaa	Cys	Xaa	Xaa	Xaa	Xaa											
		35															

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<223> Xaa is Asp or Glu

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<222> (5)...(5)

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<221> VARIANT

<222> (6)...(16)

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<222> (21)...(21)

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<222> (22)...(22)

<223> Xaa is Lys, Arg, Ile, Val, Ser or Pro

<221> VARIANT

<222> (23)...(23)

<223> Xaa is Trp, Tyr, Phe, Leu, Ile or Met

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Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Cys	Gly							
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<221> VARIANT
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<223> Xaa is Leu or Met

<221> VARIANT

<222> (14)...(14)

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<221> VARIANT

<222> (15)...(15)

<223> Xaa is Gly or Glu

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<222> (16)...(16)

<223> Xaa is Leu, Ile, Val or Pro

<221> VARIANT

<222> (17)...(17)

<223> Xaa is any amino acid

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Xaa	Gly	Cys												

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<221> misc_feature

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<223> n = A,T,C or G

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acntayccna	aycayacngt	ntgygaraar	acnathacng	tncnaargg	naarmgnytn	240
athytnmgny	tnggngayyt	ngayathgar	wsncaracnt	gygcwsnga	ytayytnytn	300
ttyacnwsnw	snwsngayca	rtayggngcn	taytgyggngw	snatgacngt	nccnaargar	360

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mgngcnwsnc	aytayytnaa	racngartay	wsnaarttyt	gyccngcngg	ntgymnggay	540
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wsnggngayw	snwsnaayaa	ycayaarccn	mgngartggy	tngarathga	yytngnggar	960
aaraaraara	thacnggnat	hmgnacnacn	ggwnsnacnc	arwsnaaytt	yaayttytay	1020
gtnaarwsnt	tygtnatgaa	ytyaaraay	aayaaywsna	artggaarac	ntayaarggn	1080
athgtnaaya	aygargaraa	rgtnttycar	ggnaaywsna	ayttymnga	yccngtnicar	1140
aayaayttya	thccnccnat	hgtngcnmgn	taygtnmng	tngtnccnca	racntggcay	1200
carmgnathg	cnytnaargt	ngarytnath	ggntgycara	thacncargg	naaygaywsn	1260
ytngtntggm	gnaaracnws	ncarwsnacn	wsngtnwsna	cnaaraarga	rgaygaracn	1320
athacnmgnc	cnathccnws	ngargaracn	wsnacnggna	thaayathac	nacngtngcn	1380
athccnytn	tnytnytn	ngtntngtn	tygcnggna	tgggnathtt	ygcngcntty	1440
mgnaaraara	araaraargg	nwsnccntay	ggwnsngcng	argncaraa	racngaytgy	1500
tggaarcara	thaaartaycc	nttygcnmgn	caycarwsng	cngarttyac	nathwsntay	1560
gayaaygara	argaratgac	ncaraarytn	gayytnatha	cnwsngayat	ggcngaytay	1620
carcarccny	tnatgathgg	nacnggnacn	gtnacnmgna	arggnwsnac	nttymgncn	1680
atggayacng	aygcngarga	rgcnggngtn	wsnacngayg	cnggnggncn	ytaygaytgy	1740
ccncarmgng	cnggnmgncn	ygartaygcn	ytncnnytn	cncncncnga	rccngartay	1800
gcnacnccna	thgtngarmg	ncaygtntytn	mgngcncaya	cnttywsngc	ncarwsnggn	1860
taymgngtnc	cnggncnca	rccnggncay	aarcaywsny	tnwsnwsngg	nggnttywsn	1920
ccngtngcng	gngtnggngc	ncargaygg	gaytaycarm	gncncayws	ngcncarccn	1980
gcngaymgng	gntaygaymg	nccnaargcn	gtnwsngcny	tngcnacnga	rwsnggncay	2040
ccngaywsnc	araarccncc	nacncayccn	ggnacnwsng	aywsntayws	ngcncnmg	2100
gaytgyytna	cncnnytnaa	ycaracngcn	atgacngcny	tnytn		2145

<210> 13

<211> 1509

<212> DNA

<213> Artificial Sequence

<220>

<223> degenerate nucleotide sequence

<221> misc_feature

<222> (1)...(1509)

<223> n = A,T,C or G

<400> 13

atgggnacng	gngcnggngg	nccnwsngtn	ytngcnytny	tnttygcngt	ntgygcncn	60
ytmgnytn	argcngarga	rytngngay	ggntgyggnc	ayathgtnac	nwsncargay	120
wsnggnacna	tgacnwsnaa	raaytayccn	ggnacntayc	cnaaytayac	ngtntgygar	180
aarathatha	cngtnccnaa	rggnaarmgn	ytnathytnm	gnytnngnga	yytnaayath	240
garwsnaara	cntgygcnws	ngaytaytn	ytnttywsnw	sngcnacnga	ycartaygg	300
ccntaytggy	gnwsntgggc	ngtnccnaar	garytnmgny	tnaaywsnaa	ygargtnacn	360
gtntnttya	arwsnggnws	ncayathwsn	ggmngngnt	tyytnytnac	ntaygcnwsn	420
wsngaycayc	cngayytnat	hacntggytn	garmngngnw	sncaytaytt	ygargaraar	480
taywsnaart	tytgycngc	nggntgymgn	gayathgcng	gngayathws	nggnaayacn	540
aargayggnt	aymgngayac	nwsnytnytn	tgyaargcng	cnathcaygc	nggnathath	600
acngaygary	tngngngnca	yathaaytn	ytncarwsna	arggnathws	ncaytaygar	660
ggnytnytn	cnaayggngt	nytnwsnmgn	cayggngwsny	tnwsngaraa	rmgnttyytn	720
tyyacnacn	cnggnatgaa	yathacnacn	gtngcnathc	cnwsngtnat	httyathgcn	780
ytnytnytna	cnggnatggg	nathttygcn	athtgymgna	armgnaaraa	raarggnaay	840
ccntaygtnw	sngcngaygc	ncaraaracn	ggntgytgga	arcarathaa	rtayccntty	900
gcnmgncayc	arwsnacnga	rttyacnath	wsntaygaya	aygaraarga	ratgacncar	960
aarytngayy	tnathacnws	ngayatggcn	gaytaycarc	arccnytnat	gathggnacn	1020
ggnacngtn	cnmgnaargg	nwsnacntty	mgncnatgg	ayacngayac	ngargargtn	1080
mgngtnaaya	cngargcnws	nggncaytay	gaytgycnc	aymgncngg	nmgncaygar	1140
taygcnytn	cnytnacnca	ywsngarccn	gartaygcna	cncnathgt	ngarmgncay	1200
ytnytnmgng	cncayacntt	ywsnacncar	wsnggntaym	ngtnccngg	nccnmgnccn	1260
acncayaarc	aywsncayws	nwsngngngn	tyccncncng	cnacngngc	nacncargtn	1320
garwsntayc	armgncngc	nwsnccnaar	ccngtnngng	gnggntayga	yaarccngcn	1380
gcnwsnwsnt	tyytngayws	nmgngayccn	gcnwsncarw	sncaratgac	nwsngngngn	1440
gaygayggnt	aywsngcncc	nmgnaaygg	ytngcncny	tnaaycarac	ngcnatgacn	1500
gcnytnytn						1509

<210> 14

<211> 1374

<212> DNA

<213> Artificial Sequence

<220>

<223> degenerate nucleotide sequence

<221> misc_feature

<222> (1)...(1374)

<223> n = A,T,C or G

<400> 14

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ytmgnytn	argcngarga	rytngngay	ggntgyggnc	ayathgtnac	nwsncargay	120

wsnggnacna	tgacnwsnaa	raaytayccn	ggnacntayc	cnaaytayac	ngtntgygar	180
aarathatha	cngtnccnaa	rggnaarmgn	ytnathytnm	gnytnngnga	yytnaayath	240
garwsnaara	cntgygcnws	ngaytayytn	ytnttywsnw	sngcnacnga	ycartaygay	300
ytnathacnt	gyytnrgarmg	nggnwsncay	tayttygarg	araartayws	naarttytgy	360
ccngcnggnt	gymngayat	hgcnggngay	athwsnggna	ayacnaarga	yggntaymgn	420
gayacnwsny	tnytntgyaa	rgcngcnath	caygcnggna	thathacnga	ygarytnngn	480
ggncayatha	ayytnytnc	rwsnaarggn	athwsncayt	aygarggnyt	nytngcnaay	540
ggngtnytnw	snmgncaygg	nwsnytnwsn	garaarmgnt	tyytnttyac	nacncnggn	600
atgaayatha	cnacngtngc	nathccnwsn	gtnathttya	thgcnytnyt	nytnacnggn	660
atgggnatht	tygcnathtg	ymgnaarmgn	aaraaraarg	gnaayccnta	ygtnwsngcn	720
gaygcncara	aracnggtg	ytggaarcar	athaartayc	cnttygcnmg	ncaycarwsn	780
acngarttya	cnathwsnta	ygayaaygar	aargaratga	cncaraaryt	ngayytnath	840
acnwsngaya	tggcngayta	ycarcarcen	ytnatgathg	gnacnggnac	ngtngcnmgn	900
aarggnwsna	cnttymgnc	natggayacn	gayacngarg	argtnmgngt	naayacngar	960
gcnwsnggnc	aytaygaytg	yccncaymgn	ccnggnmgnc	aygartaygc	nytnccnytn	1020
acncaywsng	arccngarta	ygcnacccn	athgtngarm	gncayytnyt	nmngncncay	1080
acnttywsna	cncarwsngg	ntaymgngtn	ccnggnccnm	gncnacnca	yaarcaywsn	1140
caywsnwsng	gnggnttycc	nccngcnacn	ggngcnacnc	argtngarws	ntaycarmgn	1200
ccngcnwsnc	cnaarccngt	ngngggnggn	taygayaarc	cngcngcnws	nwsnttyytn	1260
gaywsnmng	ayccngcnws	ncarwsncar	atgacnwsng	gnggngayga	yggntaywsn	1320
gcncnmgna	ayggnytngc	ncnytnaay	caracngcna	tgacngcnyt	nytn	1374

<210> 15

<211> 1001

<212> DNA

<213> Homo sapiens

<400> 15

ccgaggacca	agttaaacat	cctttaggtt	atttagctgc	acgtcctggc	ccctactctg	60
tacactagct	tctacatctg	gccgtgtacc	cacctgttca	ctgtgctcca	gctacctggc	120
cctttcctcc	ttcagcttct	ttgcacaact	tgtctgtttt	ggctcctgct	ttaatctcag	180
ctttgatgcc	acttaggcct	ttcctagctg	attcccggcc	tcacccctgt	taccgcctat	240
ctaattacag	ctctctaaat	gtgcttcaac	agcacctttc	atgtcactga	ttgcaatttg	300
cattgaatac	ttgcctgatt	atttttgtct	gcaagtgcc	catgggttta	gccctgctcc	360
tgacaagcac	actgctgaac	tgagtaactt	ttgaatgaat	gaatgaatga	gtgaataaat	420
cagtgaagg	cctacttggc	actgtcatca	tcctatcatc	aaaatatttc	gagtccctcg	480
gtgttgctat	ccctggcatg	cccattcccc	cgggctggca	aaaccctgga	gggggcagcc	540
tcccaaggca	ccgccgcggg	ctcagcccat	ctaggaatga	ctcccgcacc	acgcggcgag	600
gggcgggtcc	ggcggcgagg	tgtcctgctg	cctagcaggt	tcacgtgtac	tggtgcaggt	660
ggggaggaag	gcaaggaagg	agcgcagcag	ggcgcgccag	atacgtggag	gggagcgcgg	720
gcggcgcctc	gctcgcctcc	ggcttcgccg	tcggctactg	cctgggaacg	cgacttcctc	780
ctctaggggc	cgacgtgcgg	ggcggggcgg	ggccgggcgg	gagacgcccc	cgcagggctg	840
ggctgaaagc	cgccccaatg	ggattcggtg	cggggcagcg	actgcgcccc	gtcccggcgc	900

10003132 11501

cgcgctcgtc cgcagaggag gcggcccggc ccgggcagct gcggctcggg atccgtcgag 960
 gggaggccga gcttgccaag ctggcgccca gcggggtcat g 1001

<210> 16
 <211> 25
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> oligonucleotide primer ZC28,497

<400> 16
 ggcacatagt gacctctcag gacag 25

<210> 17
 <211> 25
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> oligonucleotide primer ZC28,498

<400> 17
 tcaatgttca aatctcccaa cctca 25

<210> 18
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> oligonucleotide primer ZC28,499

<400> 18
 ggtcgctgct cgcataggtc 20

<210> 19
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> oligonucleotide primer ZC28,500

10003132-11501

<400> 19
ctgattctga gggtgggaga ttg

1000132.11501
POSTT"ZETECOT